

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

Search for

Range: from to
 Features:
 ☐ SNP
 ☐ CDD
 ☒ MGC
 ☐ HPRD
 ☐ STS

☐ 1: [P77455](#) Reports MaoC protein (Phe...[gi:2494078])

[BLink](#),
 [Domains](#),
 [Links](#)

LOCUS P77455 681 aa linear BCT 13-SEP-2005
 DEFINITION MaoC protein (Phenylacetic acid degradation protein paaZ).
 ACCESSION P77455
 VERSION P77455 GI:2494078
 DBSOURCE swissprot: locus MAOC_ECOLI, accession [P77455](#);
 class: standard.
 extra accessions: O53009, created: Nov 1, 1997.
 sequence updated: Nov 1, 1997.
 annotation updated: Sep 13, 2005.
 xrefs: [X97452.1](#), [CAA66089.1](#), [U00096.2](#), [AAC74469.1](#), [D90777.1](#),
[BAA14997.1](#), [F64889](#)
 xrefs (non-sequence databases): EchoBASEEB3498, EcoGeneEG13735,
 InterProIPR002086, InterProIPR002539, InterProIPR011966,
 PfamPF00171, PfamPF01575, TIGRFAMsTIGR02278, PROSITEPS00070,
 PROSITEPS00687
 KEYWORDS Complete proteome; Oxidoreductase.
 SOURCE Escherichia coli
 ORGANISM [Escherichia coli](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Escherichia.
 REFERENCE 1 (residues 1 to 681)
 AUTHORS Ferrandez,A., Minambres,B., Garcia,B., Olivera,E.R., Luengo,J.M.,
 Garcia,J.L. and Diaz,E.
 TITLE Catabolism of phenylacetic acid in Escherichia coli.
 Characterization of a new aerobic hybrid pathway
 JOURNAL J. Biol. Chem. 273 (40), 25974-25986 (1998)
 PUBMED [9748275](#)
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=W / ATCC 11105
 REFERENCE 2 (residues 1 to 681)
 AUTHORS Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V.,
 Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
 Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
 Mau,B. and Shao,Y.
 TITLE The complete genome sequence of Escherichia coli K-12
 JOURNAL Science 277 (5331), 1453-1474 (1997)
 PUBMED [9278503](#)
 REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 STRAIN=K12 / MGL655
 REFERENCE 3 (residues 1 to 681)
 AUTHORS Aiba,H., Baba,T., Fujita,K., Hayashi,K., Inada,T., Isono,K.,
 Itoh,T., Kasai,H., Kashimoto,K., Kimura,S., Kitakawa,M.,
 Kitagawa,M., Makino,K., Miki,T., Mizobuchi,K., Mori,H., Mori,T.,
 Motomura,K., Nakade,S., Nakamura,Y., Nashimoto,H., Nishio,Y.,
 Oshima,T., Saito,N., Sampei,G., Seki,Y., Sivasundaram,S.,

Tagami,H., Takeda,J., Takemoto,K., Takeuchi,Y., Wada,C., Yamamoto,Y. and Horiuchi,T.

TITLE A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map

JOURNAL DNA Res. 3 (6), 363-377 (1996)

PUBMED [9097039](#)

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=K12

REFERENCE 4 (residues 1 to 681)

AUTHORS Ferrandez,A., Garcia,J.L. and Diaz,E.

TITLE Transcriptional regulation of the divergent paa catabolic operons for phenylacetic acid degradation in Escherichia coli

JOURNAL J. Biol. Chem. 275 (16), 12214-12222 (2000)

PUBMED [10766858](#)

REMARK TRANSCRIPTIONAL REGULATION.

COMMENT On May 27, 2005 this sequence version replaced [gi:7466625](#).
[PATHWAY] Phenylacetic acid aerobic catabolism.
[INDUCTION] Activated by cAMP receptor protein (CRP) and integration host factor (IHF). Inhibited by paaX.
[SIMILARITY] Belongs to the aldehyde dehydrogenase family.

FEATURES

source	Location/Qualifiers
	1..681
	/organism="Escherichia coli"
	/db_xref="taxon:562"
gene	1..681
	/gene="maoC"
	/locus_tag="b1387"
	/note="synonym: paaZ"
Protein	1..681
	/gene="maoC"
	/locus_tag="b1387"
	/product="MaoC protein"
Region	143
	/gene="maoC"
	/locus_tag="b1387"
	/region_name="Variant"
	/note="L -> V (in strain W)."
	/evidence=experimental
Site	256
	/gene="maoC"
	/locus_tag="b1387"
	/site_type="active"
	/note="By similarity."
	/evidence=not_experimental
Site	295
	/gene="maoC"
	/locus_tag="b1387"
	/site_type="active"
	/note="By similarity."
	/evidence=not_experimental
Region	440
	/gene="maoC"
	/locus_tag="b1387"
	/region_name="Variant"
	/note="A -> T (in strain W)."
	/evidence=experimental
Region	611
	/gene="maoC"
	/locus_tag="b1387"
	/region_name="Variant"

/note="S -> N (in strain W)."
/evidence=experimental

ORIGIN

```
1  mqqlasflsg twqsgrgrsr lihhaigsea lwevtsegld maaarqfaie kgapalramt
61  fieraamlka vakhllseke rfyalsagtq atradswvdi eggigtltfty aslgsrelpd
121 dtlwpedeli plskeggfaa rhlltsksgv avhinafnfp cwgmleklap twlggmpaii
181 kpatataqlt qamvksivds glvpegaisl icgsagdild hldsqudvtf tgfaatgqml
241 rvqpnivaks ipftmeads1 nccvlgedvt pdqpefal1i revvremttk agqkctairr
301 iivpqalvna vsdalvarlq kvvvgdpage gvkmgalvna eqradvqekv nillaagcei
361 rlggqadlsa agaffpptll ycpqpdetpa vhateafgpv atlmpaqnqr halqlacagg
421 gslagtlvta dpqiarqfia daarthgriq ilneesakes tghgsplpql vhgppgragg
481 geelgg1rav khymqrtavq gsptmlaais kqwvrgakve edrihpfrky feelqpgdsl
541 ltprrtmtea divnfac1sg dhfyahmdki aaaesifger vvhgyfvlsa aaglfvdagv
601 gpvianyg1e slrfiepvpk gdtiqvrltc krktlkkqrs aeekptgvve wavevfnqhq
661 tpvalysilt lvarqhgd1v d
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:19

[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[Swiss-Prot](#)Search for

UniProtKB/Swiss-Prot entry P77455

[Printer-friendly view](#)[Submit update](#)[Quick Blast](#)[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#)
[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	MAOC_ECOLI
Primary accession number	P77455
Secondary accession number	O53009
Entered in Swiss-Prot in	Release 35, November 1997
Sequence was last modified in	Release 35, November 1997
Annotations were last modified in	Release 48, September 2005
Name and origin of the protein	
Protein name	MaoC protein
Synonym	Phenylacetic acid degradation protein paaZ
Gene name	Name: maoC Synonyms: paaZ OrderedLocusNames: b1387
From	Escherichia coli [TaxID: 562]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

References

[1] NUCLEOTIDE SEQUENCE.

STRAIN=W / ATCC 11105;

DOI=10.1074/jbc.273.40.25974;MEDLINE=98421522;PubMed=9748275 [NCBI, ExPASy, EBI, Israel, Japan]

Ferrandez A., Minambres B., Garcia B., Olivera E.R., Luengo J.M., Garcia J.L., Diaz E.;
"Catabolism of phenylacetic acid in Escherichia coli. Characterization of a new aerobic hybrid pathway.";
J. Biol. Chem. 273:25974-25986(1998).

[2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=K12 / MG1655;


DOI=10.1126/science.277.5331.1453;MEDLINE=97426617;PubMed=9278503 [NCBI, ExPASy, EBI, Israel, Japan]

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J.,
Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A.,
Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).

[3] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=K12;

MEDLINE=97251357;PubMed=9097039 [NCBI, ExPASy, EBI, Israel, Japan]

Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., , Horiuchi T.;

"A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";

DNA Res. 3:363-377(1996).

[4] TRANSCRIPTIONAL REGULATION.

DOI=10.1074/jbc.275.16.12214;MEDLINE=20229831;PubMed=10766858 [NCBI, ExPASy, EBI, Israel, Japan]

Ferrandez A., Garcia J.L., Diaz E.;

"Transcriptional regulation of the divergent paa catabolic operons for phenylacetic acid degradation in Escherichia coli.";

J. Biol. Chem. 275:12214-12222(2000).

Comments

- **PATHWAY:** Phenylacetic acid aerobic catabolism.
- **INDUCTION:** Activated by cAMP receptor protein (CRP) and integration host factor (IHF). Inhibited by paaX.
- **SIMILARITY:** Belongs to the aldehyde dehydrogenase family.

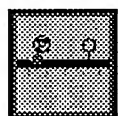
Copyright

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

Cross-references

EMBL	X97452; CAA66089.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	U00096; AAC74469.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
PIR	D90777; BAA14997.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
EchoBASE	F64889; F64889.	
EcoGene	EB3498; -.	
EcoCyc	EG13735; maoC.	
CMR	EG13735; maoC.	
InterPro	P77455; b1387.	
	IPR002086; Aldehyd_dehydrog.	
	IPR002539; MaoC_dehydratas.	
	IPR011966; PaaN-DH.	
Pfam	Graphical view of domain structure.	
	PF00171; Aldedh; 1.	
	PF01575; MaoC_dehydratas; 1.	
TIGRFAMs	Pfam graphical view of domain structure.	
PROSITE	TIGR02278; PaaN-DH; 1.	
ProDom	PS00070; ALDEHYDE_DEHYDR_CYS; FALSE_NEG.	
	PS00687; ALDEHYDE_DEHYDR_GLU; FALSE_NEG.	
HOGONOM	[Domain structure / List of seq. sharing at least 1 domain]	
BLOCKS	[Family / Alignment / Tree]	
	P77455.	

ProtoNet P77455.
 ProtoMap P77455.
 PRESAGE P77455.
 DIP P77455.
 ModBase P77455.
 SWISS-2DPAGE Get region on 2D PAGE.
 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords**Complete proteome; Oxidoreductase.****Features**

Feature table viewer

Key	From	To	Length	Description
ACT_SITE	256	256		By similarity.
ACT_SITE	295	295		By similarity.
VARIANT	143	143	1	L -> V (in strain W).
VARIANT	440	440	1	A -> T (in strain W).
VARIANT	611	611	1	S -> N (in strain W).

Sequence information

Length: **681** Molecular weight: **73003** CRC64: **A631B97AA37A1C3E** [This is a checksum on the sequence]
 AA Da

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>
MQQLASFLSG	TWQSGRGRSR	LIHHAISGEA	LWEVTSEGLD	MAAARQFAIE	KGAPALRAMT
<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>
FIERAAMLKA	VAKHLLSEKE	RFYALSAQTG	ATRADSWVDI	EGGIGTLFTY	ASLGSRELPD
<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
DTLWPEDELI	PLSKEGGFAA	RHLLTSKSGV	AVHINAFNFP	CWGMLEKLAP	TWLGGMPAII
<u>190</u>	<u>200</u>	<u>210</u>	<u>220</u>	<u>230</u>	<u>240</u>
KPATATAQLT	QAMVKSIVDS	GLVPEGAISL	ICGSAGDLLD	HLDSQDVVTF	TGSAATGQML
<u>250</u>	<u>260</u>	<u>270</u>	<u>280</u>	<u>290</u>	<u>300</u>
RVQPNIVAKS	IPFTMEADSL	NCCVLGEDVT	PDQPEFALFI	REVVREMTTK	AGQKCTAIRR
<u>310</u>	<u>320</u>	<u>330</u>	<u>340</u>	<u>350</u>	<u>360</u>
IIVPQALVNA	VSDALVARLQ	KVVVGDPAQE	GVKMGALVNA	EQRADVQEKV	NILLAAGCEI
<u>370</u>	<u>380</u>	<u>390</u>	<u>400</u>	<u>410</u>	<u>420</u>
RLGGQADLSA	AGAFFPPTLL	YCPQPDETPA	VHATEAFGPV	ATLMPAQNQR	HALQLACAGG
<u>430</u>	<u>440</u>	<u>450</u>	<u>460</u>	<u>470</u>	<u>480</u>
GSLAGTLVTA	DPQIARQFIA	DAARTHGRIQ	ILNEESAKES	TGHGSPLPQL	VHGGPGRAGG
<u>490</u>	<u>500</u>	<u>510</u>	<u>520</u>	<u>530</u>	<u>540</u>
GEELGGLRAV	KHYMQRTAVQ	GSPTMLAAIS	KQWVRGAKVE	EDRIHPFRKY	FEELQPGDSL
<u>550</u>	<u>560</u>	<u>570</u>	<u>580</u>	<u>590</u>	<u>600</u>
LTPRRTMTEA	DIVNFACLSG	DH FYAHMDKI	AAAESIFGER	VVHGYFVLSA	AAGLFVDAGV

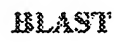
610 620 630 640 650 660
GPVIANYGLE SLRFIEPVKP GDTIQVRLTC KRKTLKKQRS AEEKPTGVVE WAVEVFNQHQ
670 680
TPVALYSILT LVARQHGDFV D

P77455 in FASTA
format

View entry in original UniProtKB/Swiss-Prot format

View entry in raw text format (no links)

Report form for errors/updates in this UniProtKB/Swiss-Prot entry

 BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-
MODEL



ExPASy Home page

Site Map

Search ExPASy

Contact us

Swiss-Prot

Hosted by  NCSC
US

Mirror
sites:

Australia Bolivia Brazil Canada Korea Switzerland Taiwan